Figure 1.   (SEQ ID NO: 1)

```
CCCGGTCGGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGAC        60
AAGGTGATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAAT       120
AATTCTATGAATTCTGTAATTTTATTCTTGATCTTTTTGAGCGAAGTTTGTTTGGGGATT       180
TTAGTTTGGTTTCCCTGTCACTGTTTTCTTTCCTTGAAACTGACTTTCATTTGCAACATG       240
AGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTGCTTAGAAGTAGTGAGAAA       300
CATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTGCCAAACTGTAGCTTTGGG       360
ATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCCTGCCTTCC       420
ATTAATTGCTTGTTTTATGAAACCACTCTTTTTTTTTTTTTTTTTTTTGGCTTCTTCA        480
TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG       540
ATGACAGTGGTACAGGAGCTCTGAATTTTTTAGATAAACTATGAGAGTGGAAACAGAAAT       600
CTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTTGTGAGAATATTTTCAAGACTACATTA       660
GTTGTGTGTTTGAGGAAAAATAAAATGTTTAAGTTGTCCATTCCTTGAAACCTCCCGACC       720
GGG                                                               723
```

Figure 2.

123bp region with identity to CHD-1
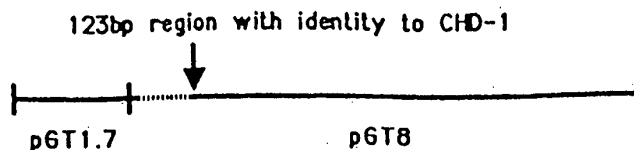
p6T1.7   p6T8

Figure 3.

```
M   CHD-1    ATTCTTCCAG ATGATCCTGA TAAAAAACCA CAAGCAAAAC AGTTACAGAC  (SEQ ID NO: 2)
C   CHD-1A   ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC  (SEQ ID NO: 3)
C   CHD-W    ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC  (SEQ ID NO: 4)
GT  CHD-W    ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC  (SEQ ID NO: 5)


M   CHD-1    CAAAAAACCA CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA
C   CHD-1A   CAAGAAACCC CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA
C   CHD-W    CAAGAAACCC CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA
GT  CHD-W    CAAGAAACCA CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA


M   CHD-1    AACTACTTAG CAGAGATCTT GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG
C   CHD-1A   AATTACTGAA TAAAGACCTT GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA
C   CHD-W    AATTACTGAA TAAAGACCTT GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA
GT  CHD-W    AATTACTGAA TAAAGACCTT GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA
```

```
M   CHD-1    ILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREAQRLCGA  (SEQ ID NO: 6)
C   CHD-1A   ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA  (SEQ ID NO: 7)
C   CHD-W    ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA  (SEQ ID NO: 8)
GT  CHD-W    ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEVQRLTGA  (SEQ ID NO: 9)
            *********************** **** * *** **
```

Figure 5.   (SEQ ID NO: 10)

```
   1  CGGGCTGCGG  CACGAAGCGC  ACCGCCGGCG  CACGCAGGCT  CGGGCCGGGG
  51  AAGGCCTGGC  CCGCCGAGCC  GGACGCACGC  AGGTATTTGG  GCAAAAATCT
 101  TGGCCATCTG  TAGAGAATAG  CAAGTCAAAC  GCATTACTTC  GAAAACATAC
 151  GGAGTACCAG  AAAGGGGATT  CTTGACCTAC  ACCTTGTAAC  CTGAGTGGAC
 201  TTTCTTTTTA  ACTTCTTAAT  ACTTACAATG  AATGGGCACA  GTGATGAAGA
 251  AAGTGTAAGA  AACAGCAGTG  GAGAGTCAAG  CAGATCAGAT  GATGATTCTG
 301  GGTCAGCTTC  AGGTTCTGGA  TCTGGTTCAA  GCTCTGGAAG  CAGTAGCGAT
 351  GGAAGTAGCA  GCCAGTCAGG  TAGCAGTGAC  TCTGAATCTG  GTTCAGAGTC
 401  AGGCAGTCAA  TCCGAATCAG  AGTCTGACAC  ATCTAGAGAG  AAGAAACAAG
 451  TTCAAGCTAA  ACCTCCGAAA  GCTGACGGAT  CTGAGTTTTG  GAAGTCCAGT
 501  CCAAGCATAC  TTGCTGTACA  GAGATCAGCA  GTGCTCAAGA  AGCAACAGCA
 551  ACAGCAAAAA  GCAGCATCAT  CAGACAGTGG  TTCAGAAGAG  GACTCATCCA
 601  GTAGTGAAGA  TTCTGCCGAT  GATTCGTCCA  GTGAAACTAA  GAAGAAAAAG
 651  CATAAAGATG  AAGACTGGCA  AATGTCAGGG  TCAGGGTCAG  TATCAGGAAC
 701  TGGTTCTGAT  TCTGAATCGG  CGGAAGATGG  GGATAAAAGC  AGTTGTGAAG
 751  AAAGTGAATC  TGACTATGAG  CCAAAAAACA  AAGTCAAAAG  CCGTAAACCT
 801  CCAAGCAGAA  TTAAGCCAAA  AAGTGGGAAA  AAGAGCACAG  GACAGAAGAA
 851  GAGGCAACTT  GATTCATCAG  AGGAGGAGGA  GGACGATGAT  GAAGATTATG
 901  ATAAGAGAGG  ATCTCGTCGC  CAGGCAACAG  TGAATGTTAG  TTACAAAGAA
 951  GCTGAAGAAA  CCAAGACAGA  TTCTGATGAT  TTGCTGGAAG  TTTGTGGAGA
1001  GGATGTCCCA  CAGACTGAAG  AAGATGAATT  TGAAACTATA  GAGAAGTTTA
1051  TGGACAGTCG  AATTGGCCGA  AAAGGAGCCA  CTGGTGCCTC  AACCACCATC
1101  TATGCCGTTG  AGGCAGATGG  TGACCCAAAT  GCTGGGTTTG  AAAAGTCAAA
1151  GGAGCTGGGA  GAAATACAGT  ATCTTATTAA  ATGGAAAGGC  TGGTCACACA
1201  TCCATAACAC  TTGGGAAACT  GAAGAAACGC  TGAAGCAACA  AAATGTTAAA
1251  GGAATGAACA  AACTGGACAA  CTACAAGAAA  AAGGATCAGG  AGACAAAACG
1301  CTGGCTGAAA  AATGCTTCTC  CAGAAGATGT  GGAATATTAT  AACTGCCAGC
1351  AGGAGCTTAC  AGATGATCTG  CACAAACAAT  ATCAAATAGT  GGAAAGAATA
1401  ATTGCTCATT  CAAATCAAAA  GTCAGCAGCT  GGTTATCCGG  ACTACTATTG
1451  CAAATGGCAG  GGTCTGCCTT  ACTCAGAATG  TAGCTGGGAA  GATGGTGCTC
1501  TCATTGCCAA  AAAGTTTCAG  GCACGCATTG  ATGAGTATTT  TAGCAGAAAT
1551  CAATCCAAGA  CTACCTCCCTT  TAAGGACTGC  AAGGTTCTAA  AACAGAGACC
1601  AAGATTGTT  GCACTGAAGA  AGCAACCATC  TTACATTGGA  GGACATGAAA
1651  GTCTGGAGTT  AAGAGATTAT  CAGTTAAATG  GATTGAATTG  GCTCGCTCAT
1701  TCATGGTGCA  AAGGAAATAG  TTGTATTCTT  GCAGATGAAA  TGGGTCTGGG
1751  TAAAACAATA  CAAACAATTT  CTTTTCTGAA  CTACCTGTTT  CATGAACATC
1801  AACTGTATGG  CCCTTTTCTT  CTGCGCGTGC  CACTTTCTAC  CTTGACATCT
1851  TGGCAAAGAG  AGATTCAAAC  TTGGGCTCCT  CAGATGAATG  CTGTAGTTTA
1901  CTTAGGAGAT  ATAACTAGTA  GAAATATGAT  AAGGACTCAT  GAATGGGATGC
1951  ATCCACAGAC  TAAACGATTA  AAGTTTAACA  TACTTCTGAC  GACATATGAA
2001  ATTTTACTGA  AGGATAAGTC  ATTCCTTGGT  GGTCTCAATT  GGGCATTCAT
2051  AGGAGTTGAT  GAAGCTCATC  GTTTAAAAAA  TGATGACTCT  CTTCTGTACA
2101  GGACTTTAAT  AGACTTTAAG  TCCAACCATC  GACTTCTGAT  TACTGGAACC
2151  CCACTGCAAA  ATTCCCTCAA  AGAGCTGTGG  TCTTTGTTGC  ATTTCATCAT
2201  GCCAGAAAAA  TTTTCCTCCT  GGGAAGATTT  TGAAGAGGAG  CATGGCAAAG
2251  GAAGAGAGTA  TGGTTATGCA  AGTCTTCACA  AAGAGCTTGA  ACCATTTTTA
2301  CTAAGAAGAG  TTAAAAAAGA  TGTAGAAAAG  TCTTTACCTG  CTAAGGTTGA
2351  ACAAATTCTG  AGGATGGAAA  TGAGTGCATT  GCAGAAGCAA  TATTACAAGT
2401  GGATTTTAAC  AAGGAATTAT  AAAGCCCTCA  GTAAAGGTTC  AAAAGGCAGT
2451  ACCTCAGGCT  TTCTGAACAT  TATGATGGAA  CTTAAGAAGT  GTTGTAACCA
2501  TTGCTACCTC  ATTAAGCCAC  CAGATGATAA  TGAATTCTAT  AATAAACAGG
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2601  AAGCTACTGA  TTCGTCTGCG  AGAACGTGGC  AACAGAGTTC  TGATTTTCTC
2651  TCAGATGGTG  AGGATGCTGG  ACATCCTAGC  AGAATATCTG  AAGTATCGCC
2701  AGTTCCCTT  CCAGAGACTT  GATGGATCAA  TAAAAGGGGA  ATTGAGGAAG
2751  CAAGCACTGG  ATCATTTCAA  TGCAGAAGGA  TCAGAGGATT  TCTGTTTTTT
2801  ACTGTCTACA  AGAGCTGGAG  GATTAGGTAT  TAACTTGGCA  TCTGCTGACA
2851  CTGTAGTTAT  TTTTGATTCT  GACTGGAATC  CACAGAATGA  TCTGCAGGCA
2901  CAGGCGAGAG  CTCATAGAAT  TGGACAGAAG  AAACAGGTTA  ATATTTATCG
2951  GCTAGTCACA  AAAGGATCAG  TAGAAGAAGA  TATTCTTGAA  AGAGCCAAGA
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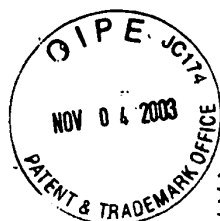
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3051 AAAACTGTTC TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTTAA
3101 TAAAGAAGAG TTATCAGCTA TTTTGAAGTT TGGTGCTGAG GAACTCTTTA
3151 AAGAACCTGA AGGAGAAGAA CAGGAGCCCC AGGAAATGGA TATAGATGAA
3201 ATCTTGAAGA GAGCTGAAAC TCGGGAAAAT GAGCCAGGTC CATTGACTGT
3251 AGGGGATGAG TTGCTTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG
3301 ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAAATTGGGAA
3351 GAAATCATCC CAGAATCCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA
3401 AAAAGAACTT GAAGAAAATAT ACATGCTCCC GAGGATGAGA AACTGTGCAA
3451 AACAGATCAG CTTTAATGGG AGTGAAGGAA GACGCAGTAG GAGCAGAAGA
3501 TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC GGCCAAAAAA
3551 GCGTGGAAGA CCTCGAACCA TTCCTCGAGA AAATATTAAA GGATTTAGTG
3601 ATGCAGAGAT CAGGCGGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT
3651 CTGGAAAGGT TAGATGCTGT AGCTAGAGAT GCTGAACTGG TTGATAAATC
3701 TGAGACAGAC CTTAGACGTT TGGGTGAACT TGTACATAAT GGATGCATTA
3751 AGGCTTTAAA GGACAATTCA TCTGGACAAG AAAGAGCAGG AGGTAGACTT
3801 GGGAAAGTTA AAGGCCCAAC GTTTCGAATC TCAGGAGTGC AGGTGAATGC
3851 AAAACTAGTC ATCTCTCACG AAGAAGAGCT GGCACCACTG CACAAATCCA
3901 TTCCTTCAGA TCCAGAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC
3951 AAGGCTGCTC ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT
4001 GTTAGTAGGC ATCTATGAAT ATGGCTATGG CAGCTGGGAA ATGATAAAAA
4051 TGGATCCAGA TCTCAGCTTA ACACAGAAGA TTTTACCTGA TGATCCAGAC
4101 AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT ACCTCATTAA
4151 ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAAGG CTTGCTGGTG
4201 CAGGCAATTC CAAGAGAAGG AAGACAAGAA ATAAGAAGAA TAAGATGAAG
4251 GCTTCAAAAA TAAAAGAAGA AATAAAGAGT GATTCTTCAC CACAACCCTC
4301 AGAAAAATCT GATGAAGATG ATGAGGAGGA GGATAACAAG GTAAATGAAA
                              * *
4351 TGAAATCTGA AAATAAAGAA AAATCTAAAA AAATTCCATT GCTGGATACT
4401 CCAGTTCATA TTACTGCAAC CAGTGAACCA GTTCCTATCT CAGAAGAATC
4451 TGAAGAACTC CATCAGAAGA CATTTAGTGT GTGCAAAGAA AGAATGAGGC
4501 CTGTCAAAGC AGCACTGAAA CAGCTGGATA GACCAGAGAA GGGGCCTTTCT
4551 GAAAGGGAGC AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGGA
4601 TCACATTACA GAATGCCTGA AGGAGTACAC AAATCCCGAG CAAAATAAAAC
4651 AGTGGAGGAA AAATTTGTGG ATTTTTGTGT CCAAGTTTAC AGAATTTGAT
4701 GCCAGAAAGC TGCACAAACT CTACAAACAT GCAATCAAAA AGCGCCAAGA
4751 GTCTCAGCAA CACAATGACC AAAACATTAG CAGCAATGTG AATACACATG
4801 TAATCAGAAA TCCAGATGTG GAAAGACTGA AGGAGACTAC AAACCATGAT
4851 GATAGTAGCA GGGACAGTTA TTCTTCTGAT AGACATTTAT CACAATACCA
4901 TGATCATCAC AAAGACAGGC ATCAGGGAGA TGCTTACAAG AAAAGTGACT
4951 CCAGGAAAAG GCCATATTCA GCCTTCAGTA ATGGAAAAGA TCACAGAGAC
5001 TGGGATCACT ACAAACAGGA CAGCAGATAC TACAGTGATA GTAAACATAG
5051 AAAGTTAGAT GACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA
5101 ACTTAAAAGA CAGCCGGGGT CATTCAGATC ACCGCTCCCA TTCAGACCAC
5151 AGGATACACT CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAATC
5201 TTCGAGAGAT TATAGATACC ACTCAGACTG GCAAATGGAC CACAGAGCTT
5251 CTGGTAGTGG CCCGAGGTCA CCACTAGATC AGAGGTCTCC TTATGGTTCA
5301 AGATCTCCCC TAGGACACAG ATCTCCATTT GAACACTCAT CAGATCACAA
5351 AAGTACACCT GAACATACAT GGAGTAGCCG GAAGACATAA CAAAGACTGA
5401 CATTTTCTGG ACCTTCTTTT TAGCCATATA CAGTAAACTA ACACAGTAAT
5451 TGCCTTACAT GACTTGAAAG ATATGGACTG GATATTCTAT CAGTAGCAGT
5501 ATTGTTACTT CTTTCCAGGA TGCAAGGTCT ATTATCCCAA CAGAAGAAAA
5551 ATATTTTGT ATTTAAAGTT TATGCTGCAC TGTGCTGCAA ATGTTGTGGC
5601 ACTTTTTTTT TAAGAAATGG AAGATGTTTA CTTTTACAGG GACCTCAACA
5651 CTGCCCCTTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG
5701 TTCTAGGCTG AACACAGATT AAATTATGTT TGTAAATGAA CACTTAAACA
5751 CTGACCTGTG CTTATGTTTC AGGAAAGAAT GGGGGATTTA TTTTGTTTTA
5801 TTTCTTGGTA GAGAACTCTC AAGGACTTTG TTCACTTTCC AAAGCTACTT
5851 GTTTACATTG TACACTGCGA CCACCTTGCC GCTTTTCATC ACAAGCTTGA
5901 ATATTTAAAT TCTGTACCTA CAGTTGTAAA ATAGCCAGGA TTTCTCCTGT
5951 TTGTGATCAG TTATAATGCC TTTTTATGAA ACAAACAAAC AAACAAAAAA
6001 CAATTAAAAA AAAAAACACA ACAAAACCAA CAAATGGCTG TAAATTATTG
6051 TAAATTAATT AAATGAGCTT TTTTCCGTCA GGCTTTTTTT GGCTGTTCCT
6101 TTCCCCAACA ACTCAGGCCT TCTTTTCACA AAGTCAGTAT ACTTACATGT
6151 TTTAATAAAA TATCTCGATG GAATCAGAAT GTAAAAATGG GGAAGGGAAT
6201 ATTTTATTCC ATTTAGTGCT CCTTTTTTAT TGGATACTTT TACATACCTG
6251 TTTTTGGTTG TTTTATTTTA TTTTTTTTTT CTATTAAACT GTCAGTGTTG
6301 TGATTGTTGT AATGAACAGT GAGAATATCC CACTCTAAAC TGTGCCCTGG
6351 AAAGCTTTTC AGGTGCATTG GTTTAAAAGA AGGAAGTGTT CTATAGGTGA
```

```
6401  ACACTTCAAA ACCCAGATCA GCCAAGATTC ATTGTAAATC CATTTGTTTT
6451  CCCTCTTTAA CATGGGCAAT AATGTCAAAT GTGCTATGCA GCAGTTAATA
6501  TTTTAGAAGA TTTGAATGAC TTTATTAACA GAATTGTTAC AATGCACACT
6551  GATTGTACAT AGATAACTTC TATCTGACAA ATTAAATTAA CTAAAACCAA
6601  AAAAAACC
```
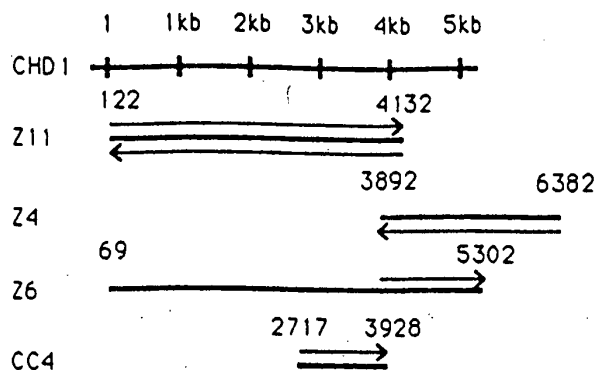
Figure 6.

Figure 7.

```
            D  E  I  V  S  V  K  H  L  H  K  K  I  K  T  E  (SEQ ID NO:  11)
CBD-1A   1  GATGAGATTGTTTCAGTGAAACATCTACATAAAAAAATAAAAACAGAAA  (SEQ ID NO:  12)
CBD-W    1  GATGGGATTGTTTCAGTGAAACATCCACATAAAAAAATAAAAGCAGAAA  (SEQ ID NO:  13)
            D  G  I  V  S  V  K  H  P  H  K  K  I  K  A  E  (SEQ ID NO:  14)

            K  E  N  E  E  K  P  E  P  D  I  G  I  K  K  E  A
CBD-1A  51  AAAGAAAATGAAGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCT
CBD-W   51  AAAGAAAATGAAGAAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCT
            K  E  N  E  E  K  D  E  P  E  I  G  I  K  K  E  A

            E  E  K  R  E  T  K  E  K  E  N  K  R  E  L  K  R
CBD-1A 101  GAAGAAAAAAGAGAGACAAAAGAGAAGGAAAATAAAAGGGAATTGAAAAGG
CBD-W  101  GGAGAAAAAAGAGAGACAAAAGAAAAGGAAAATAAGA
            G  E  K  R  E  T  K  E  K  E  N  K

            E  K  K  E  K  E  D  K  K  E  L  K  E  K  D  N  K
CBD-1A 151  GAGAAAAAAGAAAAAGAGGATAAGAAAGAATTAAAAGAAAAAGATAATAAA

            E  K  R  E  N  K  V  K  E  S  T  Q  K  E  K  E  V
CBD-1A 201  GAAAAGAGAGAAAACAAAGTAAAAGAATCCACACAGAAAGAAAAAGAAGTG

            K  E  E  K
CBD-1A 251  AAGGAAGAGAAG
```

Figure 8. (SEQ ID NO: 15)

```
ATTTATCGGC TAGTCACAAA AGGATCAGTA GAAGAAGATA TTCTTGAAAG AGCCAAGAAA AAGATGGTGT TAGATCATTT
        10         20         30         40         50         60         70         80
AGTGATTCAG AGAATGGACA CCACAGGGAA AACTGTACTA CATACAGGCT CTACTCCTTC AAGCTCAACA CCTTTTAATA
        90        100        110        120        130        140        150        160
AGGAAGAGTT ATCAGCAATT TTGAAGTTTG GTGCTGAGGA ACTTTTTAAA GAACCTGAAN NNGAAGAAGA GGAGCCTCAG
       170        180        190        200        210        220        230        240
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAAACTC GAGAAAATGA GTCAGGCCCA TTAACTGTAG GAGATGAGTT
       250        260        270        280        290        300        310        320
ACTTTCACAG TTCAAGGTAG CTAACTTTTC CAATATGGAT GAAGATGACA TTGAATTGGA ACCAGAACAA AATCTAAGAA
       330        340        350        360        370        380        390        400
ACTGGGAAGA AATCATTCCA GAAGTTCAGT GGCGACGAAT AGAGGGGNNG GAAAGACAAA AAGAACTTGA AGAAATATAT
       410        420        430        440        450        460        470        480
ATGCTTCCAA GAATGAGAAA CTGTGCAAAA CAGATCAGCT TTAATGGAAA TGAAGGGAGA TGCAGTAGGA GCAGAAGATA
       490        500        510        520        530        540        550        560
TTCTGGATCT GATAGTGATT CCATCTCAGA AAGAAAACGA CCAAAAAAAC GTGGACGACC ACGAACTATT CCCCGTGAAA
       570        580        590        600        610        620        630        640
ACATTAAAGG ATTTAGTGAT GCAGAGATTA GACGATTTAT CAAGAGTTAC AAGAAATTTG GTGGCCCAGT TGAAAGGTTA
       650        660        670        680        690        700        710        720
GATGCTATAG CTAGAGATGC TGAGCTAGTT GATAAATCTG AAACAGACCT TAGACGTCTG GGAGAACTTG TACATAATGG
       730        740        750        760        770        780        790        800
ATGCATTAAG GCTTTAAATG ATAATGACTT TGGTCAAGGA AGAACAGGTG GTAGATTTGG GAAAGTTAAA GGCCCAACAT
       810        820        830        840        850        860        870        880
TCCGAATAGC AGGAGTGCAG GTGAATGCAA AGCTAGTCAT TTCTCACGAA GAAGAGTTGG CACCATTGCA TAAATCGATT
       890        900        910        920        930        940        950        960
CCTTCAGATC CAGAAGAAAG GAAAAGATAT GTCATCCCAT ACCACACCAA AGCAGCTCAT TTTGATATAG ATTGGGGTAA
       970        980        990       1000       1010       1020       1030       1040
AGAAGATGAT TCCAATCTGT TAATAGGCAT CTATGAATAT GGTTATGGCA GTTGGGAAAT GATAAAAATG GATCCTGATC
      1050       1060       1070       1080       1090       1100       1110       1120
TCAGTTTGAC ACAGAAGATT TTACCTGATG ATCCAGATAA GAAACCCCAG GCTAAGCAGT TACAGACTCG TGCAGATTAC
      1130       1140       1150       1160       1170       1180       1190       1200
CTCATTAAAT TACTGAATAA AGACCTTGCA AGAAAGGAAG CACAGAGACT TGCTGGTGCA GGCAATTCAA AGAGGAGAAA
      1210       1220       1230       1240       1250       1260       1270       1280
AACAAGAAGT AAGAAGAATA AAGCAACAAA GGCTGC
      1290       1300       1310
```

Figure 9.

```
                                                                        $
C CHD-1A    DARRYLGKNLGHL*RIASQTHYFENIRSTRKGILDLHLVT*VDFLFNFLILTMNGHSDEE (SEQ ID NO: 16)
M CHD-1     FALCPPVTQREPQETRECRKFIFEILIFEEICIHTHLLLIGDFCFINFLIFTMNGHSDEE (SEQ ID NO: 17)
                                                              ********

C CHD-1A    SVRNSSGESSRSDDDSAGSASGSGSGSSSSGSSSDGSSSQSGSSDSESGSESGSQSESESD
M CHD-1     SVRNGSGESSQSGDD-CGSASGSGSGSSSSGSSSDGSSSQSGSSDSDSGSDSGSQSESESD
            ****  ***** *  **  ************************ *.*** .**********

C CHD-1A    TSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAVLKKQQQQ---QKAASSDSGSEEDSS
M CHD-1     TSRENK-VQAKPPKVDGAEFWKSSPSILAVQRSAMLRKQPQQAQQQRPASSNSGSEEDSS
            ****.* ****** ** .**************** .* ** **    *. .**.*******

C CHD-1A    SSEDSADDSSSETKKKKHKDEDWQMSGSGSVSGTGSDSESAEDGDKSSCEESESDYEPKN
M CHD-1     SSEDS-DDSSSGAKRKKHNDEDWQMSGSGSPSQLGSDSESEEERDKSSCDGTESDYEPKN
            ***** ***** .*.***.*********** * ******* *.***** .********

C CHD-1A    KVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEEDDDEDYDKRGSRRQATVNVSYKEAEE
M CHD-1     KVRSRKPQNRSKSKNGKKILGQKKRQIDSSEDEDDEDYDNDKRSSRRQATVNVSYKEDEE
            **.****  .* *.*.*** .*****.***.*.*.* * ***.*************** **

C CHD-1A    TKTDSDDLLEVCGEDVPQTEEDEFETIEKFMDSRIGRKGATGASTTIYAVEADGDPNAGF
M CHD-1     MKTDSDDLLEVCGEDVPQPEDEEFETIERVMDCRVGRKGATGATTTIYAVEADGDPNAGF
            ***************** *..******. ** *.********.**.************.***

           .KTXEPGEIQYLIKWKGWSHIHNTWETEETLKQQNVRGMKKLDNYKKKDQETKRWLKNAS
C CHD-1A    EKSKELGEIQYLIKWKGWSHIHNTWETEETLKQQNVRGMKKLDNYKKKDQETKRWLKNAS
M CHD-1     ERNKEPGDIQYLIKWKGWSHIHNTWETEETLKQQNVRGMKKLDNYKKKDQETKRWLKNAS
           *..** *.*********************************.** .*************

HUMAN       PEDVEYYNCQQELTDDLHKQYQIVERTNXSFQSKSAAGYP     (SEQ ID NO: 18)
C CHD-1A    PEDVEYYNCQQELTDDLHKQYQIVERIIAHSNQKSAAGYPDYYCKWQGLPYSECSWEDGA
M CHD-1     PEDVEYYNCQQELTDDLHKQYQIVERIIAHSNQKSAAGLPDYYCKWQGLPYSECSWEDGA
            ************************* **.**********  ***************.****

C CHD-1A    LIAKKFQARIDEYFSRNQSKTTPFKDCKVLKQRPRFVALKKQPSYIGGHESLELRDYQLN
M CHD-1     LISKKFQTCIDEYFSRNQSKTTPFKDCKVLKQRPRFVALKKQPSYIGGHEGLELRDYQLN
            ** .****. ***********************************.******* *******

C CHD-1A    GLNWLAHSWCKGNSCILADEMGLGKTIQTISFLNYLFHEEQLYGPFLLRVPLSTLTSWQR
M CHD-1     GLNWLAHSWCKGNSCILADEMGLGKTIQTISFLNYLFHEEQLYGPFLLVVPLSTLTSWQR
            ********************************************** .***********

C CHD-1A    EIQTWAPQMNAVVYLGDITSRNMIRTHEWMHPQTKRLKFNILLTTYEILLKDKSFLGGLN
M CHD-1     EIQTWASQMNAVVYLGDINSRNMIRTHEWMHPQTKRLKFNILLTTYEILLKDKAFLGGLN
            ******.***********.****************************** .******.******

C CHD-1A    WAFIGVDEAHRLKNDDSLLYRTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSS
M CHD-1     WAFIGVDEAHRLKNDDSLLYKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSS
            ******************* .***************************************

C CHD-1A    WEDFEEEHGKGREYGYASLHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALQKQYYK
M CHD-1     WEDFEEEHGKGREYGYASLHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALQKQYYK
            ************************************************************

C CHD-1A    WILTRNYKALSKGSKGSTSGFLNIMMELKKCCNHCYLIKPPDDNEFYNKQEALQHLIRSS
M CHD-1     WILTRNYKALSKGSKGSTSGFLNIMMELKKCCNHCYLIKPPDNNEFYNKQEALQHLIRSS
            ****************************************** .*****************

C CHD-1A    GKLILLDKLLIRLRERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQAL
M CHD-1     GKLILLDKLLIRLRERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQAL
            ************************************************************
```

```
C CBD-1A    DHFNAEGSEDFCFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQV
M CBD-1     DHFNAEGSEDFCFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQV
            ************************************************************

C CBD-W     -IYRLVTKGSVEEDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSTPSSSTPFNKEELSA (SEQ ID NO: 19)
C CBD-1A    NIYRLVTKGSVEEDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSAPSSSTPFNKEELSA
M CBD-1     NIYRLVTKGSVEEDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSTPSSSTPFNKEELSA
            ***********************************************.************

C CBD-W     ILKFGAEELFKEPEXEEEEPQEMDIDEILKRXETRENESGPLTVGDELLSQFKVANFSNM
C CBD-1A    ILKFGAEELFKEPEGEEQEPQEMDIDEILKRAETHENEPGPLSVGDELLSQFKVANFSNM
M CBD-1     ILKFGAEELFKEPEGEHQEPQEMDIDEILKRAETRENEPGPLTVGDELLSQFKVANFSNM
            ***********************************..***.***.***.***********

C CBD-W     DEDDIELEPEQNLRNWEHIIPEVQWRRIEGXERQKELEEIYHLPRMRNCARDISFNGNEG
C CBD-1A    DEDDIELEPERNSKNWEHIIPEEQRRRLEEEERQKELEEIYHLPRMRNCARDISFNGSEG
M CBD-1     DEDDIELEPERNSRNWEHIIPESQRRRIEEEERQKELEEIYHLPRMRNCARDISFNGSEG
            **********.*.*.******* *.**.*  ***********************.**.**

C CBD-W     RCSRSRRYSGSDSDSISERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPVER
C CBD-1A    RRSRSRRYSGSDSDSISERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLER
M CBD-1     RRSRSRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLER
            * ************.*.***********************************.**

C CBD-W     LDAIARDAELVDKSETDLRRLGELVHNGCIKALNDNDFGQGRTGGRFGKVKGPTFRIAGV
C CBD-1A    LDAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSSGTERAGGRLGKVKGPTFRISGV
M CBD-1     LDAVARDAELVDKSETDLRRLGELVHNGCIKALKDNSSGQERAGGRLGKVKGPTFRISGV
            ***.************************.***.*.**.* * *.***.********.***

C CBD-W     QVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPYHTKAAHFDIDWGKEDDSNLLIGIYH
C CBD-1A    QVNAKLVIAHDELIPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLLIGIYH
M CBD-1     QVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSNLLVGIYH
            ********.**.**.************.**.*.**.*.** *****************.****

C CBD-W     YGYGSWEMIKMDPDLSLTQKILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAG
C CBD-1A    YGYGSWEMIKMDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREAQRLCG
M CBD-1     YGYGSWEMIKMDPDLSLTQKILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAG
            ******************.***************************..***..*****.*

C CBD-W     AGNSKRRKTRSKKNKATKAA
C CBD-1A    AGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDD----KLNDSKPESKDRS
M CBD-1     AGNSKRRKTRNKKNK-MKASKIKEEIKSDSSPQPSEKSDEDDEEEDNKVNEMKSENKEKS
            ** ******* **.*  *       ***** ********.    *.*. *.*.*..*

C CBD-1A    KKSVVSDAPVHITASGEPVPIAEESEELDQKTFSICKERMRPVKAALKQLDRPEKGLSER
M CBD-1     KKIPLLDTPVHITATSKPVPISEESEELHQKTFSVCKERMRPVKAALKQLDRPEKGLSER
            **  .*.******..*****.*****.****.*********************

C CBD-1A    EQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKRTHFDARKLHKLYKHAI
M CBD-1     EQLEHTRQCLIKIGDHITECLKEYTNPEQIKQWRKNLWIFVSKRTHFDARKLHKLYKHAI
            ************************.***********************************

C CBD-1A    KKRQESQQNSDQN-SNVATTHVIRNPDMERLKENTNHDDSSRDSYSSDRHLSQYHDHHKD
M CBD-1     KKRQESQQHNDQNISSNVMTHVIRNPDVERLKHTTNHDDSSRDSYSSDRHLSQYHDHHKD
            *****..**.*** *.  ********.****.*.************************

C CBD-1A    RHQGDSYKKSDSRKRPYSSFSNGKDHREWDHYRQDSRYYSDREHRKLDDHRSREHRPSL.
M CBD-1     RHQGDAYKKSDSRKRPYSAFSNGKDHRDWDHYKQDSRYYSDS-KHRKLDDHRSRDHRSNL
            *****.************.*.*******.****.*******.. *********.**..*

C CBD-1A    EGGLKD-RCHSDHRSHSDHRMHSDHRSTPSTHIINPPRDYRYLSDWQLDHRAASSGPRSP
M CBD-1     EGNLKDSRGHSDHRSHSDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSP
            ** *** *..********** *********.....*.*****.***.****..******

                                              $
C CBD-1A    LDQRSPYGSRSP------FEHSAEHRSTPEHTWSSRKTXQKLMSLSSGTLFXP
M CBD-1     LDQRSPYGSRSPLGHRSPFEHSSDHKSTPEHTWSSRKTXQRLTFSGPSFXPYTVNXHSNC
            ************      ****..*.**************.*. *.*. .*

C CHD-1A    LTXLERYGLDILSVAVLLLLSRMQGLLSQQKKNIFVFKVYAALCCKCCGTFFLRNGRCLL
C CHD-1A    LQGPQHCPFQTGSYYKTLHVKVVLGXTQIKLCLXHNTXTLTCAYVSGKNGGFILFYFLVH
C CHD-1A    NSQGLCSLSKATCLHCTLRPPCRFSSQAXIFKFCTYSCKIARISPVCDQLXCLFMKQTNK
C CHD-1A    QKTIKKXNTTKPTNGCKLLXINXMSFFPSGFFWLFLSPTTQAFFSQSQYTYHFXXNISMH
C CHD-1A    SECKNGEGNILFBLVLLFYWILLHTCMLFYFIFFYXTVSVVIVVHNSENIPLXTVPWK
C CHD-1A    AFQVHWFKRRKCSIGZHFKTQISQDSLXIHLFSLFNMGNNVKCAHQQLIFXXIXMTLLTH
C CHD-1A    LLQCTLIVHRXLLSDKLNXLKPKXT
```

Figure 10.

```
  55 KPPKADGSEFWKSSPSILAVQRSAVLKKQQQQQKAASSDSGSEEDSSSSE 104 (SEQ ID NO: 20)
     .::|. :.|.:.. |.:.::.||    .:....:|..  .||:.|:|    |
2654 MAAKDISTEVLQN.PELYGLRRS...HRAAAHQQNYFNDSDDEDD....E 2695 (SEQ ID NO: 21)

 105 DSADDSSSETKKKKHKDEDWQMSGSGSVSGTGSDSESAEDGDKSSCEESE 154
     |.. .:|.... ...||       ...:.::|:||:|....|| ||:.
2696 DNIKQSRRKRMTTIEDDED.......EFEDEEGEEDSGEDEDEEDFEEDD 2738

 155 SDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEEDDDEDYDKR 204
     . |:... |  ...||.||.|.|| .|.:.:|..:|       .:
2739 DYYGSPIKQNRSKPKSRTKSKSKSKPKSQSEKQSTVKIP........TRF 2780

 205 GSRRQATVNVSYKEAEETKTDSDDLLE....VCGEDVPQT....EEDEFE 246
     :.|.. |||  ... .::. :|:| .:   ::.:|:|.:.   :.::|.
2781 SNRQNKTVNYNIDYSDDDLLESEDDYGSEEALSEENVHEASANPQPEDFH 2830

 247 TIEKFMDSRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKW 296
     .|: .:: |:         .|.: .... :.. ::::|:|   :.::||||
2831 GIDIVINHRL........KTSLEEGKVLEKTVPDLNNCKE..NYEFLIKW 2870

 297 KGWSHIHNTWETEETLKQQNVKGMNKLDNYKKK...DQETKRWLKNASPE 343
     .: ||:|||||||  |.: |   |:|:.:|||| |.   ::: |: ...:|
2871 TDESHLHNTWETYESIGQ..VRGLKRLDNYCKQFIIEDQQVRLDPYVTAE 2918

 344 DVEYYNCQQELTDDLHKQYQIVERIIA..HSNQKSAAGYPDYYCKWQGLP 391
     |:|. : :.|   |  .:::.||||.  :.. ..:.: :|..||. |
2919 DIEIMDMERERRLDEFEEFHVPERIIDSQRASLEDGTSQLQYLVKWRRLN 2968

 392 YSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKDCKVLKQRPRFVALK 441
     |.|..||::. |.|   .|:| .|:.||. . .|||||| |.
2969 YDEATWENATDIVKLAPEQVKHFQNRENSKILPQYSSNYTSQRPRFEKLS 3018

 442 KQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLGKTIQTI 491
     ||.:|  |    ||||:||.|:||:| |:||:...||||||||||||:||:
3019 VQPPFIKGG...ELRDFQLTGINWMAFLWSKGDNGILADEMGLGKTVQTV 3065

 492 SFLNYLFHEHQLYGPFLLRVPLSTLTSWQREIQTWAPQMNAVVYLGDITS 541
     .|:..|:  .:.  || :: |||||:..|  .:::.||||::|.:.|:|: .|
3066 AFISWLIFARRQNGPHIIVVPLSTMPAWLDTFEKWAPDLNCICYMGNQKS 3115

 542 RNMIRTHEW....MHPQTKRLKFNILLTTYEILLKDKSFLGGLNWAFIGV 587
     |: ||..|:     . ...| :|||:||||||.:|||. ||::|.|.|:|
3116 RDTIREYEFYTNPRAKGKKTMKFNVLLTTYEYILKDRAELGSIKWQFMAV 3165

 588 DEAHRLKNDDSLLYRTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPE 637
     |||||||||.:| || .| .|| .:|:||||||||.:||| .|::|:||:
3166 DEAHRLKNAESSLYESLNSFKVANRMLITGTPLQNNIKELAALVNFLMPG 3215

 638 KFSSWEDFE.EEHGKGREYGYASLHKELEPFLLRRVKKDVEKSLPAKVEQ 686
     :|. :::: |:::.:.|  . .||: ::||:|||:||||||||||||.|.|.
3216 RFTIDQEIDFENQDEEQEEYIHDLHRRIQPFILRRLKKDVEKSLPSKTER 3265

 687 ILRMEMSALQKQYYKWILTRNYKALSKGSKGSTSGFLNIMMELKKCCNHC 736
     |||:|:|.:|.:|..||| |||:||  |||:||.|| |.|.| ::|||||.:||.
3266 ILRVELSDVQTEYYKNILTKNYSALTAGAKGGHFSLLNIMNELKKASNHP 3315

 737 YLIKPPDDNEF.......YNKQEALQHLIRSSGKLILLDKLLIRLRERGN 779
     ||:. :::. :          .:::.|. ||.|||||:|||.||.||:. |:
3316 YLFDNAEERVLQKFGDGKMTRENVLRGLIMSSGKMVLLDQLLTRLKKDGH 3365
```

```
 780 RVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGS  829
     |||||||||||||||||::||..:.: ||||||.:.:. |: .:||||..:|
3366 RVLIFSQMVRMLDILGDYLSIKGINFQRLDGTVPSAQRRISIDHFNSPDS  3415

 830 EDFCFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKK  879
     :||.|||||||||||||| .||||||||||||||.||| ||||||||||.
3416 NDFVFLLSTRAGGLGINLMTADTVVIFDSDWNPQADLQAMARAHRIGQKN  3465

 880 QVNIYRLVTKGSVEEDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSTPS  929
     :| :|||||.|:.||:::|||||:||||:||||:. :| |.|. .....
3466 HVMVYRLVSKDTVEEEVLERARKKMILEYAIISLGVTDGNKYTKKNEP..  3513

 930 SSTPFNKEELSAILKFGAEELFKEPEGEEQEPQEMDIDEILKRAETRENE  979
     | :|||||||||||:::|...: ::.. :::::|::|.:||.: ..
3514 .....NAGELSAILKFGAGNMFTATD.NQKKLEDLNLDDVLNHAEDHVTT  3557

 980 PG...PLTVGDELLSQFKVANFSNMDEDDIELEPERNSRNWEEIIPESQR  1026
     |: .|:|:|.||.|.:: :..: :|:::||||.:
3558 PDLGESHLGGEEFLKQFEVTDY............KADIDWDDIIPEEEL  3594

1027 RRIEEEERQKELEE.....IYMLPRMRNCAKQI..SFNGSE.........  1060
     ::::::||..:. || : |: |. |. |.| |.||.:
3595 RKLQDEEQRRKDEEYVKEQLEMMNRRDNALKKIKNSVNGDGTAANSDSDD  3644

1061 ..GRRSRSRRYSGSDSDSITERKRPKKRGRPRTIPR.ENIKGFSD...AE  1104
     ..||..|| .:.| |||.| .. |: :.| : :|:|:: | |:
3645 DSTSRSSRRRARANDMDSIGE...SEVRALYKAILKFGNLKEILDELIAD  3691

1105 IRRFIKSYKKFGGPLERLDAVARDA.........ELVDKSETDLRRLGEL  1145
     :||:.|:|::..: ..|:|. |:::| |::.|
3692 GTLPVKSFEKYGETYDEMMEAAKDCVHEEEKNRKEILEKLEKHATAYRAK  3741

1146 VHNGCIKALKD.NSSGQERAGGRLGKVKGPTFRISGVQ.VNAKLVISHEE  1193
     :..| ||| .: ....| : : . |:. |.:.|| :||. ::|: |
3742 LKSGEIKAENQPKDNPLTRLSLKKREKKAVLFNFKGVKSLNAESLLSRVE  3791

1194 ELAPLHKSIPSD.PEERKRYVIPCHTKAA..HFDIDWGKEDDSNLLVGIY  1240
     :| |..| | |: .::. :: :. :|. : /::. :|.||:|..||:|::
3792 DLKYLKNLINSNYKDDPLKFSLGNNTPKPVQNWSSNWTKEEDEKLLIGVF  3841

1241 EYGYGSWEMIKMDPDLSLTQKILPDD......................  1266
     .||||||. |: || ::|:||: ::
3842 KYGYGSWTQIRDDPPLGITDKIFLNEVHNPVAKKSASSSDTTPTPSKKGK  3891

1267 .....PDKKPQAKQLQTRADYLIKLLNKDLARK......EAQRLAGAGNS  1305
     ..| |.| :|. |.|||:.:|. :|. | :..:|:..:...
3892 GITGSSKKVPGAIHLGRRVDYLLSFLRGGLNTKSPSADIGSKKLPTGPSK  3941

1306 KRRKTRNKKNKMKASKIKEEIKSDSSPQPSEKSDEDDEE...EDNKVNEM  1352
     ||.:......| ....|... ..::.| .. |.:... ::.:|..
3942 KRQRKPANHSKSMTPEITSSEPANGPPSKRMKALPKGPAALINNTRLSPN  3991

1353 KSENKEKSKKIPLLDTPVHITATSEPVPISEESEELHQKTFSVCKERMRP  1402
     ... . ||| . :|. ..|:|. |....|... |:. |..:
3992 SPTPPLKSKVSRDNGTR....QSSNPSSGSAHEKEYDSMDEEDCRHTMSA  4037

1403 VKAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITECLKEYTNPEQIKQ  1452
     :|..||.| |.:|:|. :| . : |..||:|| |: |: .... ..
4038 IRTSLKRLRRGGKSLDRKEWAKILKTELTTIGNHI.ESQKGSSRKASPEK  4086

1453 WRKNLWIFVSKP..TEFDARKLHKLYKHAIKKRQESQQ  1488
     :||:|| : ..| .:..:. || :| .| |||.
4087 YRKHLWSYSANFWPADVKSTKLMAMY....DKITESQK  4120
```

Figure 11.

```
CCBD   AVEAD| GDPNAGFEKSKELGE.IQYLIKWKGWSHIBNTWETEET| LRQQNVKGMNKLDNYKK  (SEQ ID NO:  22)
MCBD   AVEAD| GDPNAGFERNKEPGD.IQYLIKWKGWSHIBNTWETEET| LRQQNVRGNKKLDNYKK  (SEQ ID NO:  23)
YCBD   EGKVL| EKTVPDLNNCKE..N.YEFLIKWTDESBLBNTWETYES| IGQ..VRGLKRLDNYCK  (SEQ ID NO:  24)
             **       ****   **  ****** *   *  *  *   **** *
DBP1   EEEEE| YAVEKIIDRRVRKGK.VEYYLKWKGYPETENTWEPENN| LDCQDLIQQY  (SEQ ID NO:  25)
BBP1   EDEEE| YVVEKVLDRRVVKGKQVEYLLKWKGFSEEBNTWEPEKN| LDCPELISEF  (SEQ ID NO:  26)
MMOD1  EEEEE| YVVEKVLDRRVVKGK.VEYLLKWKGFSDEDNTWEPEEN| LDCPDLIAEF  (SEQ ID NO:  27)
MMOD2  AEPEE| FVVEKVLDRRVVNGK.VEYFLKWKGFTDADNTWEPEEN| LDCPELIBDF  (SEQ ID NO:  28)
             **   ***  ****  **  *** *****      ****** *  ***   **
DPC    PVDLV| YAAEKIIQKRVKKGV.VEYRVKWKGWNQRYNTWEPENN| ILDRRLIDIY  (SEQ ID NO:  29)
MMOD3  VGEQV| FAAECILSKRLRKGK.LEYLVKWRGWSSKBNSWEPEEN| ILDPRLLLAF  (SEQ ID NO:  30)
            *   *** *  **  ***   **  ***  **    *  **** *  ******
                                      ^^       ^ ^^
```

Figure 14.

```
MOUSE     CBD1      AGA TAT TCT GGA TCT GAT AGT GAT TCA ATC TCG GAA (SEQ ID NO: 31)
CHICKEN   CBD-1A    --- --- --- --- --- --- --- --C --C --- A-A --- (SEQ ID NO: 32)
SPIX      CBD-1A                                 C --C --- --- --- (SEQ ID NO: 33)
CHICKEN   CBD-W     --- --- --- --- --- --- --- --- --C --- --A --- (SEQ ID NO: 34)
SPIX      CBD-W                                  C --C --- --A --- (SEQ ID NO: 35)
HYACINTH  CBD-W         -- --- --- --- --C --C --- --A --- (SEQ ID NO: 36)
P1                  A TAT TCT GGA TCT GAT AGT GAY TC  (SEQ ID NO: 37)
P3                  AGA TAT TCC GGA TCT GAT AGT GA    (SEQ ID NO: 38)


MOUSE     CBD1      AGG AAA CGG CCG AAG AAA CGT GGG CGA CCC CGC ACT
CHICKEN   CBD-1A    --A --- --- --A --A --G --- --A A-- --T --A --C
SPIX      CBD-1A    --- --- --- --A --A --G --- --A A-- --A --A ---
CHICKEN   CBD-W     --A --- --A --A --A --- --- --A --- --A --A ---
SPIX      CBD-W     --A --- --A --A -GA --- --- --A --- --A --A ---

HYACINTH  CBD-W     --A --- --A --A -GA --- --- --A --- --A --A ---


MOUSE     CBD1      ATC CCT CGG GAG AAT ATT AAA GGA TTT AGT GAT GCG GAG
CHICKEN   CBD-1A    --T --- --A --A --- --- --- --- --- --- --- --A ---
SPIX      CBD-1A    --T --- --A --A --- --A
CHICKEN   CBD-W     --T --C --T --A --C --- --- --- --- --- --- --A ---
SPIX      CBD-W     --T --- --T --A --- ---
P2                                          TTT CCT AAA TCG CTA CGT CT (SEQ ID NO: 39)
HYACINTH  CBD-W     --- --- --- --- --- --- --- --- --- --C --- --A --G
HYACINTH  CBD-W     ATT AGG CGG T
```